Fig. 1

Interaction between IgE and its high affinity receptor

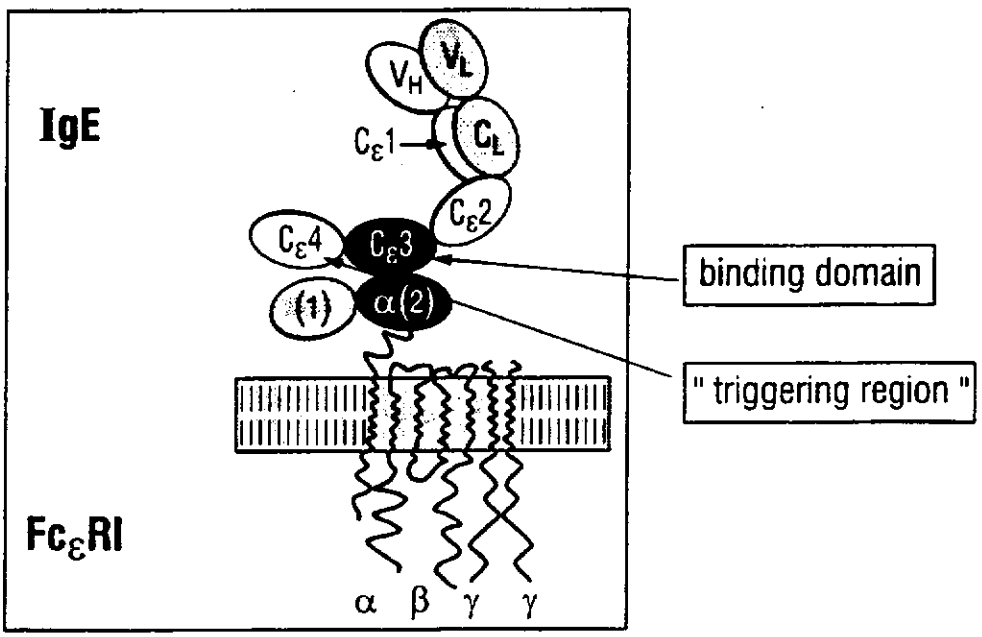
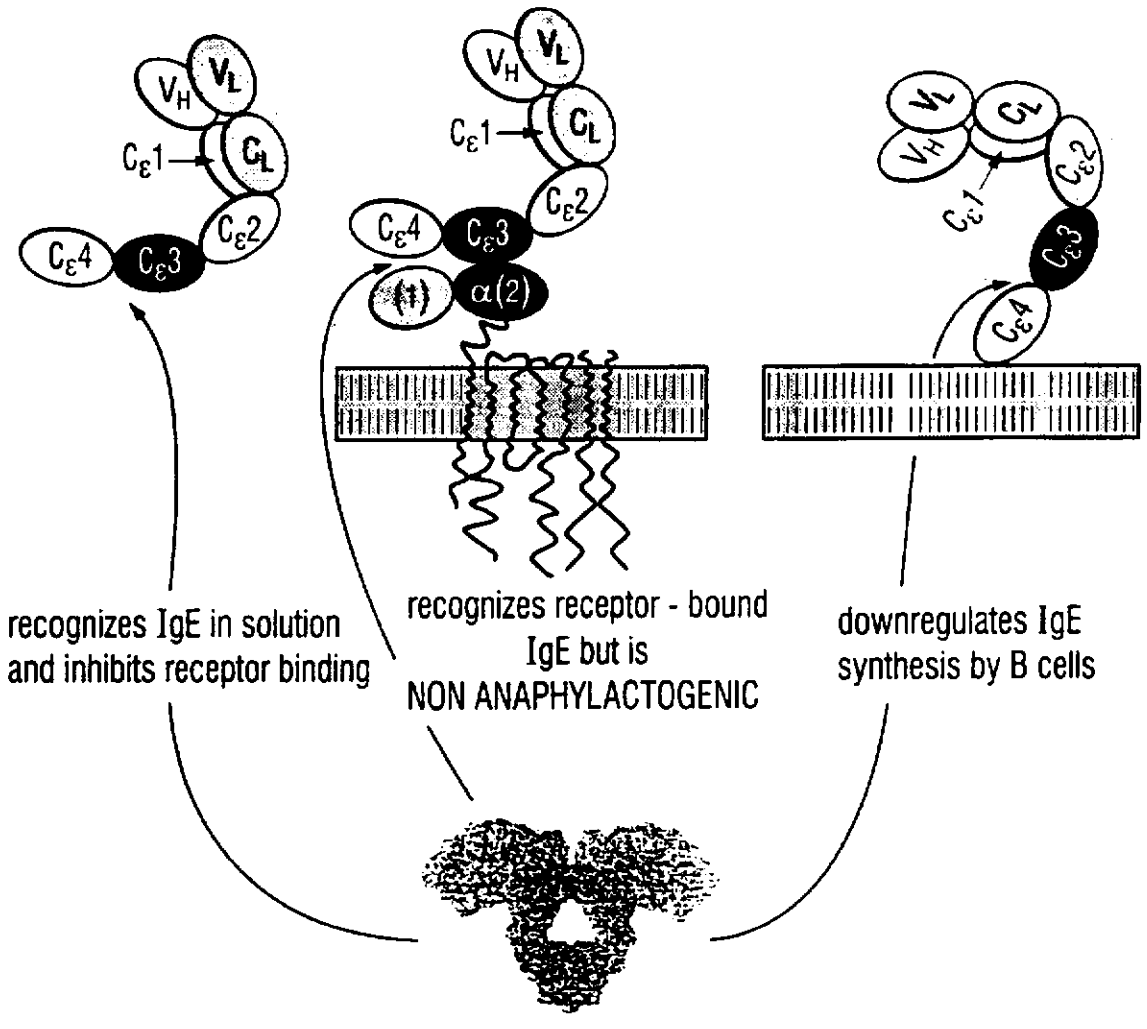


Fig. 2

Properties of the monoclonal anti-hIgE antibody BSW17



BSW17

Fig. 3

The anti-idiotypic network

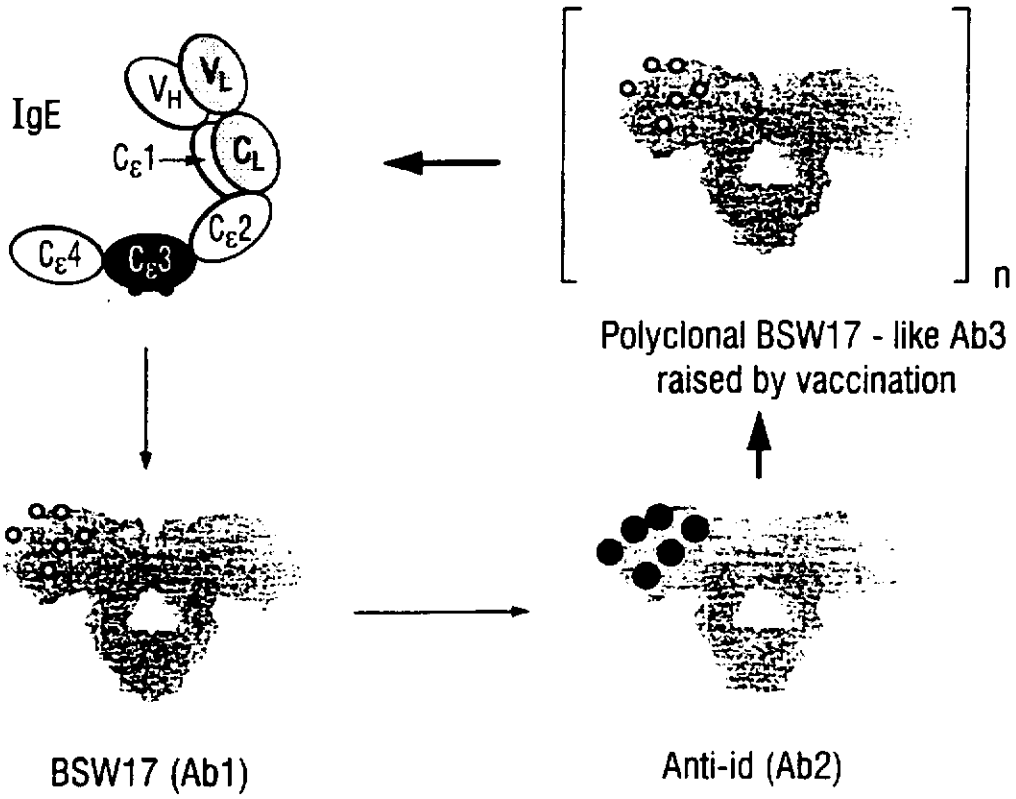


Fig. 4

Schematic structure of recombinant mimobodies

Fig.4A

Anti-id-BSW17.52; light chain

$(L.C.)_2$

Fig.4B

Anti-id-BSW17.52; Fab

F_{AB}

Fig.4C

Anti-id-BSW17.43; Fab

F_{AB}

Fig. 5a

Anti-BSW17 Fab clone 52: variable heavy chain: DNA sequence of bacteriophage-displayed human immunoglobulin and deduced amino acid sequence. Hypervariable regions (Complementarity Determining Regions; CDR) are shown in italics.

5′	CAG	GTG	9 AAA	CTG	CTC	18 GAG	TCG	GGG	27 GGA	GGC	CTG	36 GTC	AAG	CCT	45 GGG	GGG	TCC	54 CTG
	Q	V	K	L	L	E	S	G	G	G	L	V	K	P	G	G	S	L
	AGA	CTC	63 TCC	TGT	GCA	72 GTC	TCT	GGA	81 TTC	ACC	TTC	90 AGT	CDR1 *AAC*	*TAT*	99 *AAT*	*ATG*	*AAC*	108 TGG
	R	L	S	C	A	V	S	G	F	T	F	S	*N*	*Y*	*N*	*M*	*N*	W
	GTC	CGC	117 CAG	GCT	CCA	126 GGG	AAG	GGA	135 CTA	GAG	TGG	144 GTC	TCA	CDR2 *TCC*	153 *ATT*	*AGT*	*AGT*	162 *CGA*
	V	R	Q	A	P	G	K	G	L	E	W	V	S	*S*	*I*	*S*	*S*	*R*
	AAT	*TCT*	171 *TAC*	*ATA*	*TAC*	180 *TAC*	*GCA*	*GAC*	189 *TCA*	*GTG*	*AAG*	198 *GGC*	CGA	TTC	207 ACC	ATC	TCC	216 AGA
	N	*S*	*Y*	*I*	*Y*	*Y*	*A*	*D*	*S*	*V*	*K*	*G*	R	F	T	I	S	R
	GAC	AAC	225 GCC	GAG	AGT	234 ACC	TTG	TAT	243 CTG	CAA	ATG	252 GAC	AAC	CTG	261 GGA	GTC	GAA	270 GAC
	D	N	A	E	S	T	L	Y	L	Q	M	D	N	L	G	V	E	D
	ACG	GCT	279 GTC	TAT	TTT	288 TGT	ACG	AGC	CDR3 *GGC*	*CGC*	*CTT*	306 *TTC*	*GAC*	*TAC*	315 TGG	GGC	CAG	324 GGA
	T	A	V	Y	F	C	T	S	*G*	*R*	*L*	*F*	*D*	*Y*	W	G	Q	G
	ACC	CTG	333 GTC	ACC	GTC	342 TCC	TCT	3′										
	T	L	V	T	V	S	S											

14 OCT 2003

Fig. 5b

Anti-BSW17 Fab clone 52: variable light chain: DNA sequence of bacteriophage-displayed human immunoglobulin and deduced amino acid sequence. Hypervariable regions (Complementarity Determining Regions; CDR) are shown in italics.

5′	GTG V	ATG M	9 ACC T	CAG Q	TCT S	18 CCA P	TCC S	TCA S	27 CTG L	TCT S	GCA A	36 TCT S	GTA V	GGA G	45 GAC D	AGA R	GTC V	54 ACC T
	ATC I	ACT T	63 TGT C	**CDR1** ***CGG*** ***R***	***GCT*** ***A***	72 ***AGT*** ***S***	***CAG*** ***Q***	***GGC*** ***G***	81 ***ATT*** ***I***	***AAC*** ***N***	***AAT*** ***N***	90 ***TAT*** ***Y***	***TTA*** ***L***	***GCC*** ***A***	99 TGG W	TTT F	CAG Q	108 CAG Q
	AAA K	CCA P	117 GGG G	AAA K	GCC A	126 CCT P	AAG K	TCC S	135 CTG L	ATC I	TAT Y	**CDR2** ***AGT*** ***S***	***GCA*** ***A***	***TCC*** ***S***	153 ***ATT*** ***I***	***TTG*** ***L***	***CAA*** ***Q***	162 ***AGT*** ***S***
	GGG G	GTC V	171 CCA P	TCC S	AAG K	180 TTC F	AGC S	GGC G	189 AGT S	GGA G	TCT S	198 GGG G	ACA T	GAT D	207 TTC F	ACT T	CTC L	216 ACC T
	ATC I	AGC S	225 AAC N	CTG L	CAG Q	234 CCT P	GAA E	GAT D	243 TTT F	GCA A	ACT T	252 TAT Y	TAC Y	TGC C	**CDR3** ***CAA*** ***Q***	***CAA*** ***Q***	***TAT*** ***Y***	270 ***AAT*** ***N***
	TAT ***Y***	***TAT*** ***Y***	279 ***CCG*** ***P***	***CTC*** ***L***	***ACT*** ***T***	288 TTC F	GGC G	GGA G	297 GGG G	ACC T	AAG K	306 GTG V	GAG E	ATC I	315 AAA K	3′		

Fig. 5c

Anti-BSW17 Fab clone 43: variable heavy chain: DNA sequence of bacteriophage-displayed human immunoglobulin and deduced amino acid sequence. Hypervariable regions (Complementarity Determining Regions; CDR) are shown in italics.

5′	CAG	GTG	9 AAA	CTG	CTC	18 GAG	TCG	GGC	27 CCA	GGA	CTG	36 GTG	AAG	CCT	45 TCG	GAG	ACC	54 CTG
	Q	V	K	L	L	E	S	G	P	G	L	V	K	P	S	E	T	L
	TCC	CTC	63 ACC	TGC	ACT	72 GTC	TCT	GGT	81 GGC	TCC	ATC	CDR1 ***AGC***	***AGT***	***GGT***	99 ***GGT***	***TAC***	***TAC***	108 ***TGG***
	S	L	T	C	T	V	S	G	G	S	I	***S***	***S***	***G***	***G***	***Y***	***Y***	***W***
	ACC	TGG	117 ATC	CGC	CAG	126 CGC	CCA	GGG	135 AAG	GGC	CTG	144 GAG	TGG	ATT	CDR2 ***GGA***	***TAC***	***ATC***	162 ***TAT***
	T	W	I	R	Q	R	P	G	K	G	L	E	W	I	***G***	***Y***	***I***	***Y***
	TAC	***AGT***	171 ***GGG***	***AGC***	***ACC***	180 ***TCC***	***TAC***	***AAC***	189 ***CCG***	***TCC***	***CTC***	198 ***AAG***	***AGT***	CGA	207 GTC	ACC	ATG	216 TCA
	Y	***S***	***G***	***S***	***T***	***S***	***Y***	***N***	***P***	***S***	***L***	***K***	***S***	R	V	T	M	S
	GTG	GAC	225 ACG	TCT	AAA	234 AAC	CAG	TTC	243 TCC	CTG	AGG	252 CTG	ACC	TCT	261 GTG	ACT	GCC	270 GCG
	V	D	T	S	K	N	Q	F	S	L	R	L	T	S	V	T	A	A
	GAC	ACG	279 GCC	GTC	TAT	288 TAC	TGT	GCG	297 CGA	CDR3 ***GAG***	***CGG***	306 ***GGT***	***GAG***	***ACC***	315 ***GGT***	***CTA***	***TAT***	324 ***TAC***
	D	T	A	V	Y	Y	C	A	R	***E***	***R***	***G***	***E***	***T***	***G***	***L***	***Y***	***Y***
	CCC	***TAT***	333 ***TAC***	***TAC***	***ATA***	342 ***GAC***	***GTC***	TGG	351 GGC	ACA	GGG	360 ACC	ACC	GTC	369 ACC	GTC	TCC	378 TCA
	P	***Y***	***Y***	***Y***	***I***	***D***	***V***	W	G	T	G	T	T	V	T	V	S	S

3′

Fig. 5d

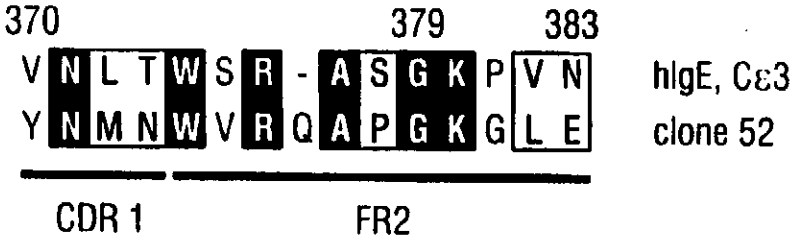
Anti-BSW17 Fab clone 43: variable light chain: DNA sequence of bacteriophage-displayed human immunoglobulin and deduced amino acid sequence. Hypervariable regions (Complementarity Determining Regions; CDR) are shown in italics.

5′	GAG	CTC	9 GTG	GTG	ACT	18 CAG	CCT	GCC	27 TCC	GTG	TCT	36 GGG	TCT	CCT	45 GGA	CAG	TCG	54 ATC
	E	L	V	V	T	Q	P	A	S	V	S	G	S	P	G	Q	S	I
	ACC	ATC	63 TCC	TGC	**CDR1** ***ACT***	72 ***GGA***	***ACC***	***AGA***	81 ***AGT***	***GAC***	***GTT***	90 ***GGT***	***GGT***	***TAT***	99 ***AAC***	***TAT***	***GTC***	108 ***TCC***
	T	I	S	C	***T***	***G***	***T***	***R***	***S***	***D***	***V***	***G***	***G***	***Y***	***N***	***Y***	***V***	***S***
	TGG	TAC	117 CAA	CAA	CAC	126 CCA	GGC	AAA	135 GCC	CCC	AAA	144 CTC	ATG	ATT	153 TAT	**CDR2** ***GAT***	***GTC***	162 ***AGT***
	W	Y	Q	Q	H	P	G	K	A	P	K	L	M	I	Y	***D***	***V***	***S***
	AAT	***CGG***	171 ***CCC***	***TCA***	GGG	180 GTT	TCT	AAT	189 CGC	TTC	TCT	198 GGC	TCC	AAG	207 TCT	GGC	AAC	216 ACG
	N	***R***	***P***	***S***	G	V	S	N	R	F	S	G	S	K	S	G	N	T
	GCC	TCC	225 CTG	ACC	ATC	234 TCT	GGG	CTC	243 CAG	GCT	GAG	252 GAC	GAG	GCT	261 GAT	TAT	TAC	270 TGC
	A	S	L	T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y	C
	CDR3 ***AGC***	***TCA***	279 ***TAT***	***ACA***	***AGC***	288 ***AGC***	***AGC***	***ACT***	297 ***CTC***	***GGG***	***GTG***	306 TTC	GGC	GGA	315 GGG	ACC	AAG	324 TTG
	S	***S***	***Y***	***T***	***S***	***S***	***S***	***T***	***L***	***G***	***V***	F	G	G	G	T	K	L
	ACC	GTC	333 CTA	GGT	CAG	342 CCC	3′											
	T	V	L	G	Q	P												

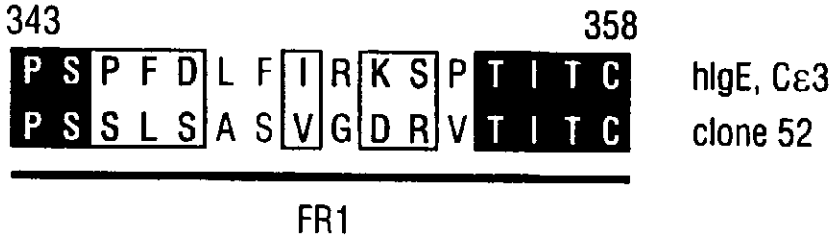
Fig. 6A

Amino acid sequence homology between anti-BSW17 rFab and the Cε3 domain of human IgE

Anti-Id Fab, clone 52; **heavy chain**:



Anti-Id Fab, clone 52; **light chain**; alignment 1:



Anti-Id Fab, clone 52; **light chain**; alignment 2:

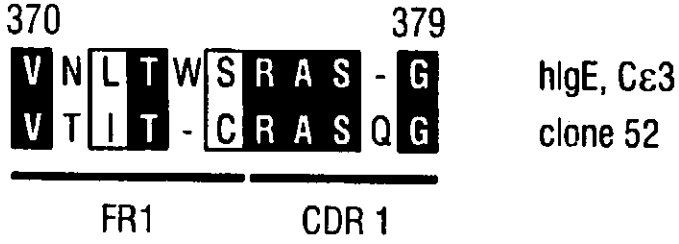
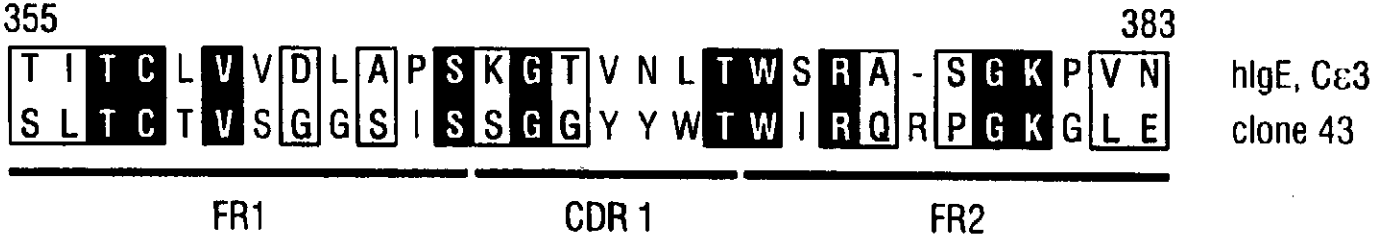


Fig. 6B

Amino acid sequence homology between anti-BSW17 rFab and the Cε3 domain of human IgE

Anti-Id Fab, clone 43; **heavy chain**:



Anti-Id Fab, clone 43; **light chain**:

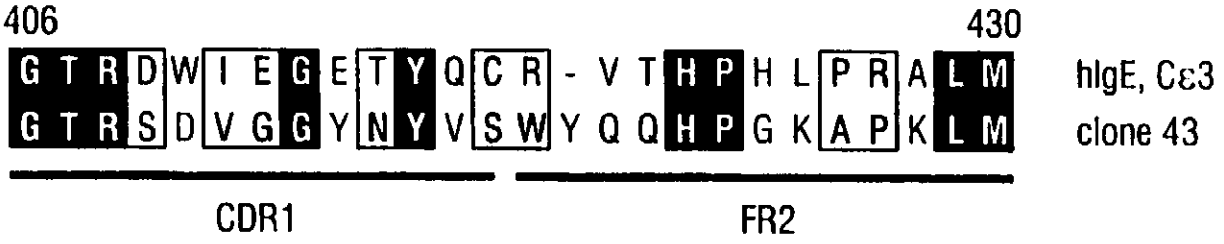


Fig. 7

Competitive binding of anti- id BSW17 rFab on IgE-primed CHOα cells with FITC-labeled BSW17

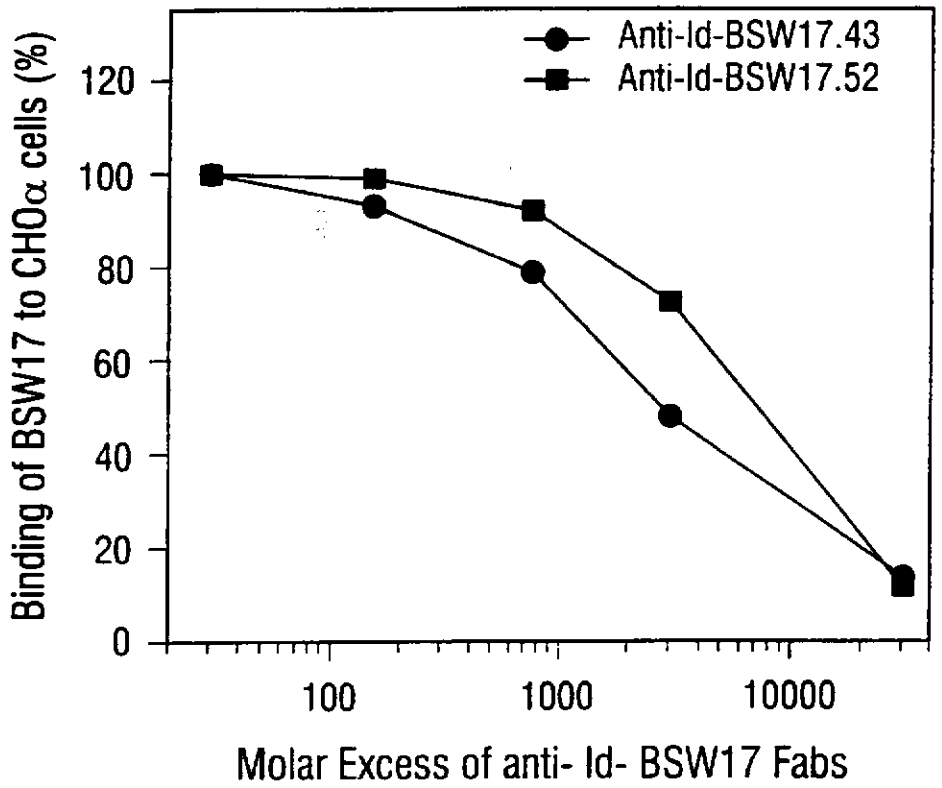


Fig. 8

Binding of affinity-purified rabbit anti-BSW17 mimobody immunoglobulins to human IgE

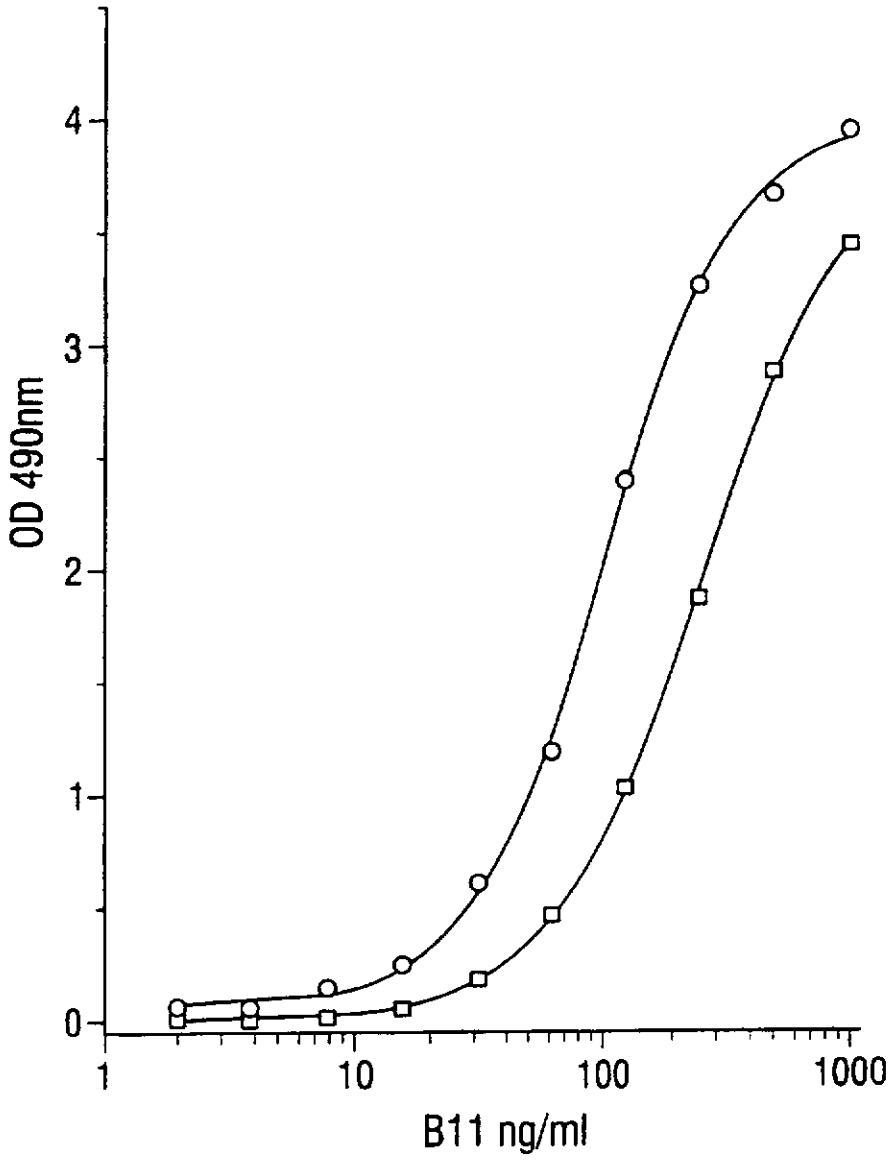


Fig. 9 Anti-BSW17 mimobody immune response in Balb/c mice

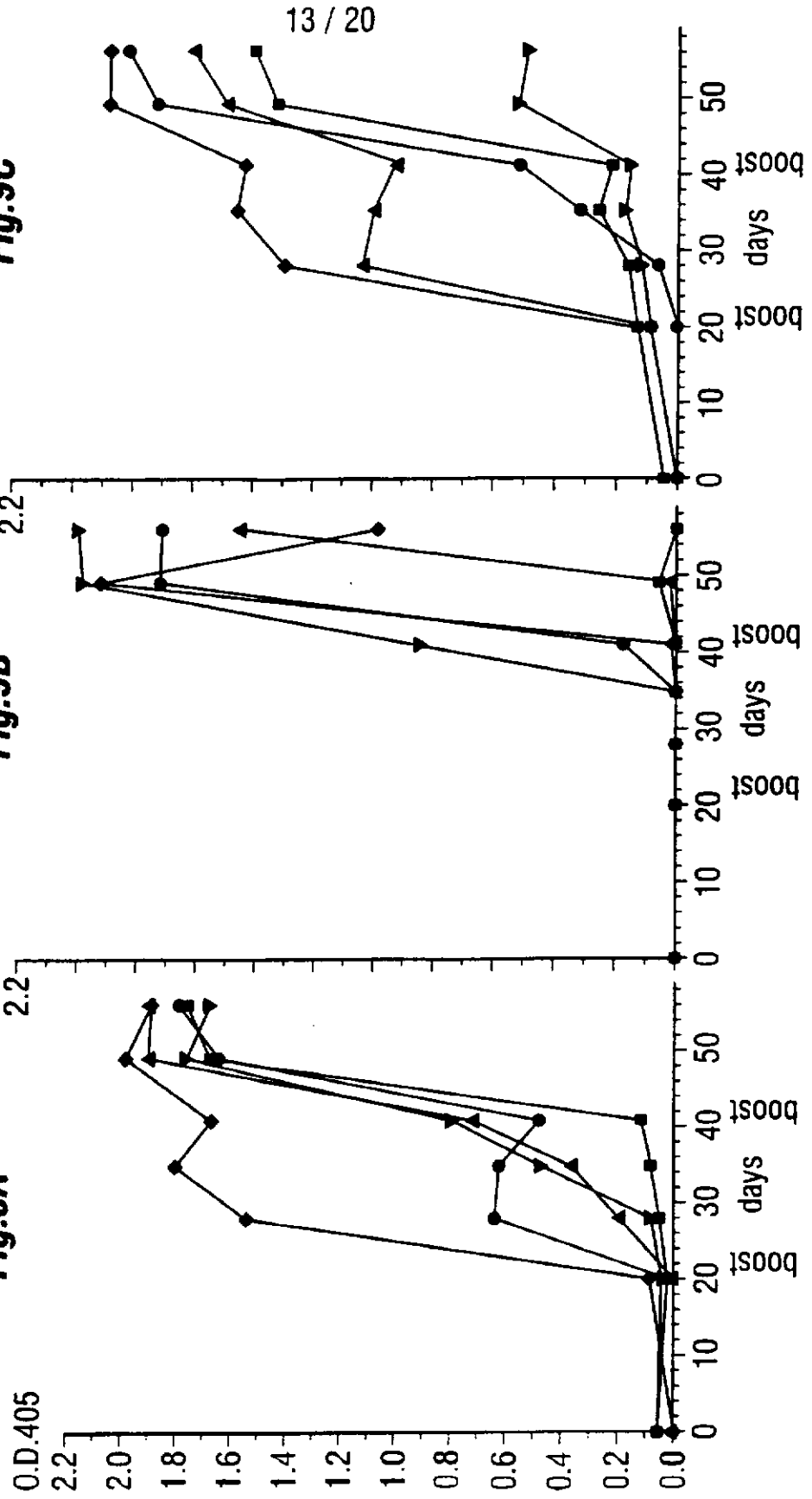


Fig. 10 Inhibition of hIgE / FcεRIα binding by immunoaffinity-purified anti-mimobody antibodies

Fig. 10A

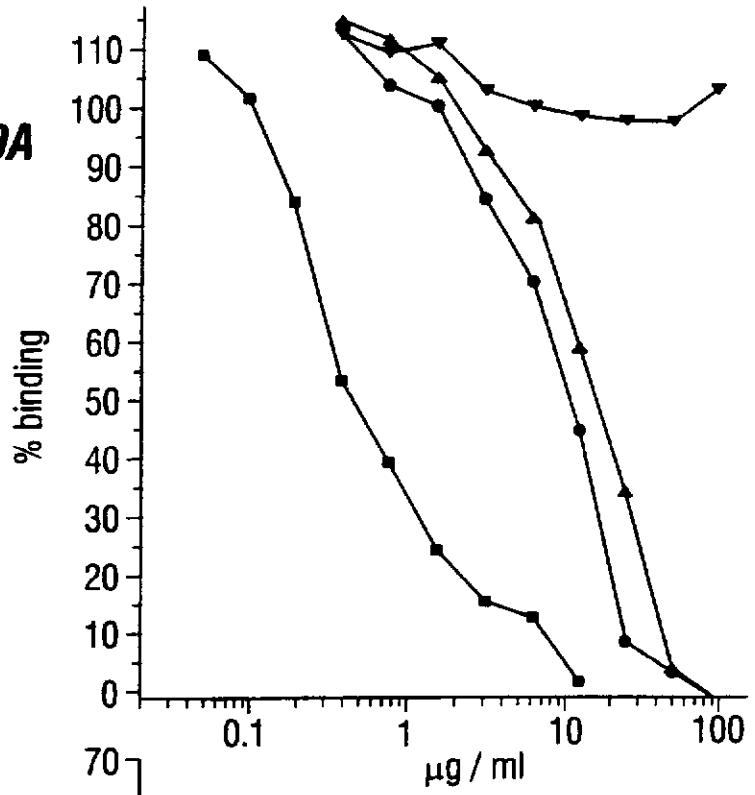


Fig. 10B

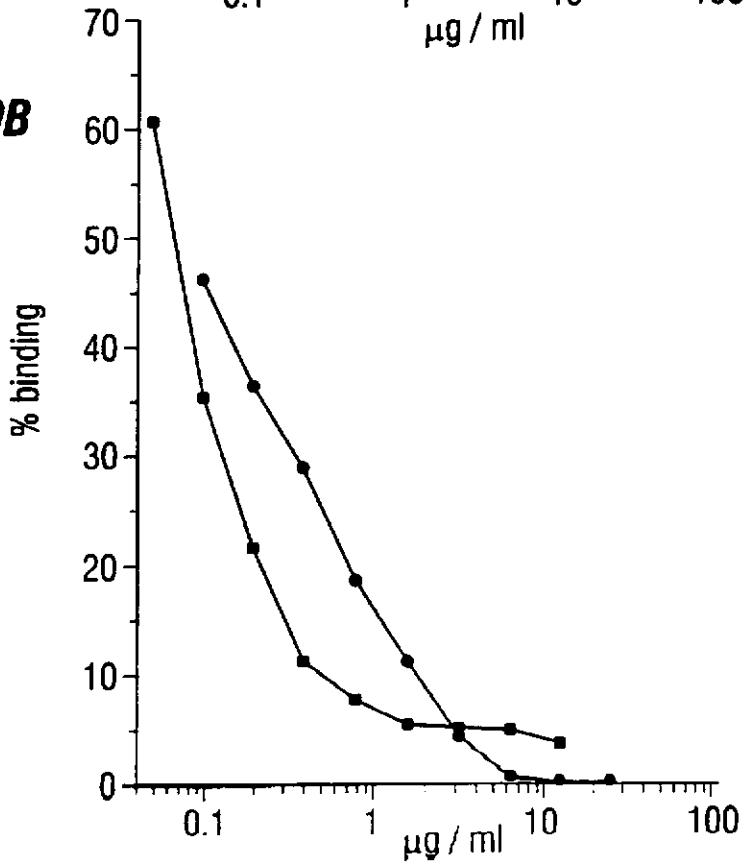


Fig. 11

PCA score profiles of rhesus monkey groups (n = 2), immunized with different mimobody preparations

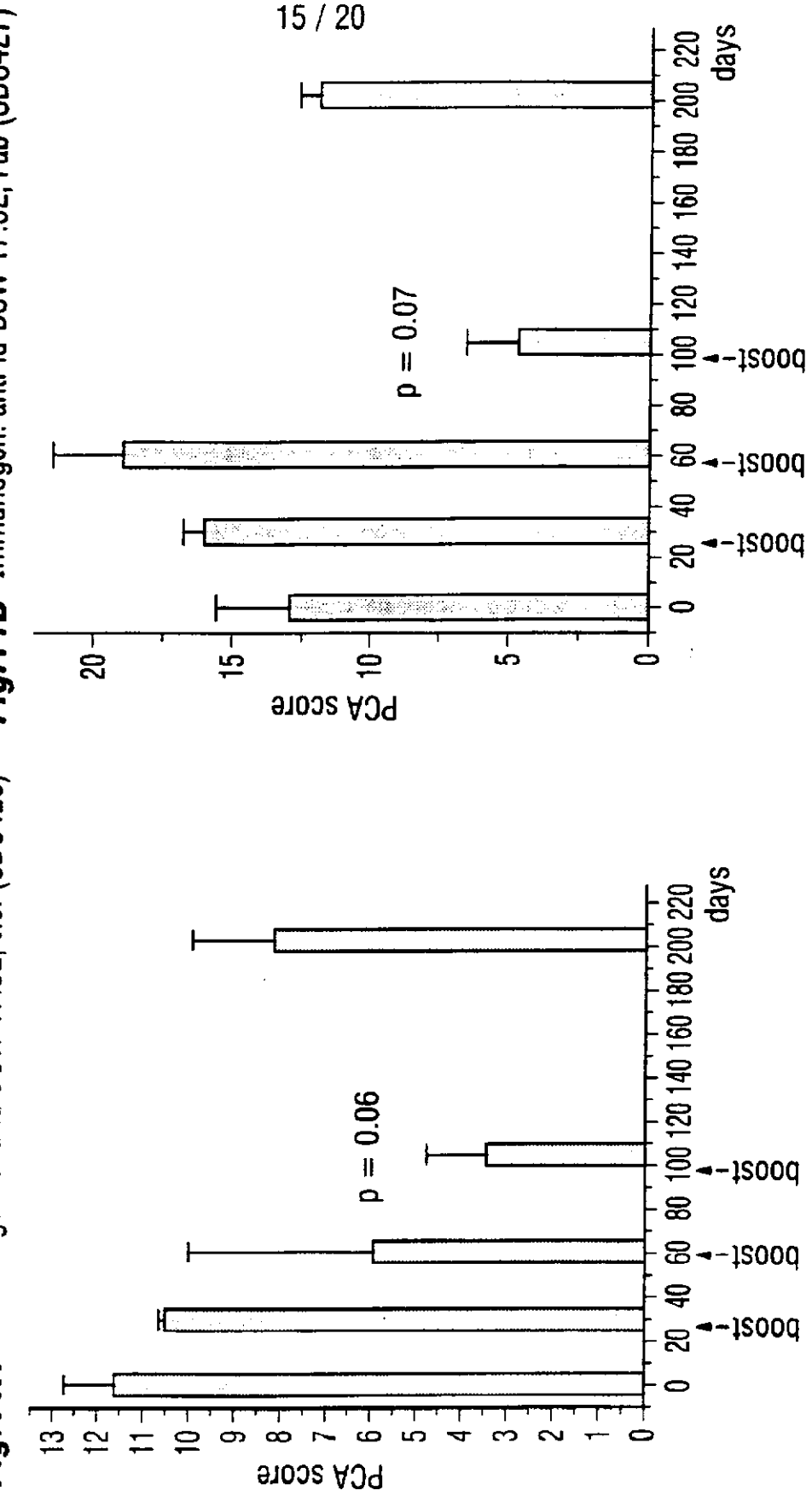


Fig.11A Immunogen: anti-id-BSW 17.52; i.c. (SDS426) ***Fig.11B*** Immunogen: anti-id-BSW 17.52; Fab (SDS427)

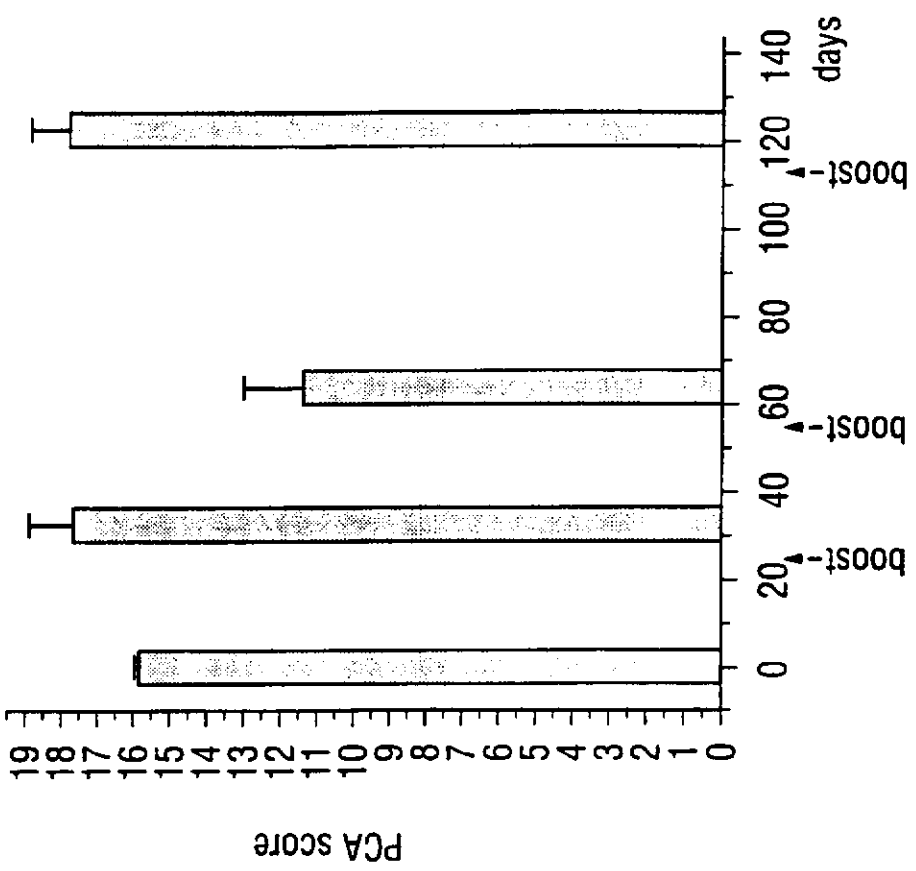


Fig.11C Immunogen: anti-id-BSW 17.43; Fab (SDS463)

Fig. 12a

Anti-BSW17 Fab clone 52: variable and first constant domain of heavy chain

Q	V	K	L	L	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	V	S
G	F	T	F	S	N	Y	N	M	N	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	S
I	S	S	R	N	S	Y	I	Y	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A
E	S	T	L	Y	L	Q	M	D	N	L	G	V	E	D	T	A	V	Y	F	C	T	S	G	R
L	F	D	Y	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S	V	F	P
L	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V	K	D	Y	F	P	E
P	V	T	V	S	W	N	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S
G	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V
N	H	K	P	S	N	T	K	V	D	K	K	A	E	P	K	S	C							

Fig. 12b

Anti-BSW17 Fab clone 52: variable and constant domain of kappa light chain

V M T Q S P S S L S A S V G D R V T I T C R A S Q
G I N N Y L A W F Q Q K P G K A P K S L I Y S A S
I L Q P G V P S K F S G S G T D F T L T I S S
E Q P E D F A T Y Y C Q Q Y N Y Y P L T F G G G T
R V E I K T V A A P S V F I F P P S D E Q L K S G
T A S V V C L L N N F Y P R E A K V Q W K V D N A
L Q S G N S Q E S V T E Q D S K D S T Y S L S S
L T L S K A D Y E K H K V Y A C E V T H Q G L S
P V T K S F N R G E C

Fig. 12c

Anti-BSW17 Fab clone 43: variable and first constant domain of heavy chain

Q V K L L E S G P G L V K P S E T L S L T C T V S
G G S I S S G G Y Y T W W I R Q R P G K G L E W I
G Y I Y Y S G S T S Y N P S L K S R V T M S V D T
S K N Q F S L R L T S V T A A D T A V Y Y C A R E
R G E T G L Y Y P Y Y Y I D V W G T G T T V T V S
S A S T K G P S V F P L A P S S K S T S G G T A A
L G C L V K D Y F P E P V T V S W N S G A L T S G
V H T F P A V L Q S S G L Y S L S S V V T V P S S
S L G T Q T Y I C N V N H K P S N T K V D K K A E
P K S C

Fig. 12d

Anti-BSW17 Fab clone 43: variable and constant domain of lambda light chain

E	L	V	V	T	Q	P	A	S	V	S	G	S	P	G	Q	S	I	T	I	S	C	T	G	T
R	S	D	V	G	G	Y	N	Y	V	S	W	Y	Q	Q	H	P	G	K	A	P	K	L	M	I
Y	D	V	S	N	R	P	S	G	V	S	N	R	F	S	G	S	K	S	G	N	T	A	S	L
T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y	C	S	S	Y	T	S	S	S	T	L	G
V	F	G	G	G	T	K	L	T	V	L	G	Q	P	Q	P	K	A	A	P	S	V	T	L	F
P	P	S	S	E	E	L	Q	A	N	K	A	T	L	V	C	L	I	S	D	F	Y	P	G	A
V	T	V	A	W	K	A	D	S	S	P	V	K	A	G	V	E	T	T	T	P	S	K	Q	S
N	N	K	Y	A	A	S	S	Y	L	S	L	T	P	E	Q	W	K	S	H	K	S	Y	S	C
Q	V	T	H	E	G	S	T	V	E	K	T	V	A	P	T	E	C	S						